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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=2; day=17; hr=17; min=39; sec=12; ms=182; ]

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Application No: 10585499 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2009-01-28 09:53:06.559  
**Finished:** 2009-01-28 09:53:07.676  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 117 ms  
**Total Warnings:** 7  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 17  
**Actual SeqID Count:** 17

Error code	Error Description
E 201	Mandatory field data missing in <141>
W 402	Undefined organism found in <213> in SEQ ID (2)
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W 402	Undefined organism found in <213> in SEQ ID (13)
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W 402	Undefined organism found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)

SEQUENCE LISTING

<110> The Government of the United States as represented by the  
Secretary, Department of Health and Human Services

<120> COMPOSITIONS AND METHODS FOR THE HIGH EFFICIENCY EXPRESSION OF  
THE TRANSFORMING GROWTH FACTOR-BETA SUPERGENE FAMILY

<130> NIHA-0282

<140> 10585499

<141> 2009-01-28

<150> PCT/US2005/00378

<151> 2005-01-06

<150> US 60/534,379

<151> 2004-01-06

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 390

<212> PRT

<213> Homo sapiens

<400> 1

Met Pro Pro Ser Gly Leu Arg Leu Leu Leu Leu Leu Pro Leu Leu  
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr  
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala  
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser  
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu  
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu  
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu  
100 105 110

Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr  
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val  
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu  
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn  
165 170 175

Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser  
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu  
195 200 205

Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser  
210 215 220

Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr  
225 230 235 240

Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro  
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln  
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser  
275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys  
290 295 300

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn  
305 310 315 320

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr  
325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala  
340 345 350

Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr  
355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val  
370 375 380

Arg Ser Cys Lys Cys Ser  
385 390

<210> 2  
<211> 390  
<212> PRT  
<213> Sus scrofa scrofa

<400> 2

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu  
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr  
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala  
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser  
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu  
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu  
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu  
100 105 110

Met Leu Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro  
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val

130	135	140
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu		
145	150	155
Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn		
165	170	175
Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser		
180	185	190
Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu		
195	200	205
Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser		
210	215	220
Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn		
225	230	235
240		
Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro		
245	250	255
Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His		
260	265	270
Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser		
275	280	285
Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys		
290	295	300
Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn		
305	310	315
320		
Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr		
325	330	335
Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala		
340	345	350
Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr		
355	360	365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val  
370 375 380

Arg Ser Cys Lys Cys Ser  
385 390

<210> 3  
<211> 414  
<212> PRT  
<213> Homo sapiens

<400> 3

Met His Tyr Cys Val Leu Ser Ala Phe Leu Ile Leu His Leu Val Thr  
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Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe  
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu  
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Glu Glu Val Pro  
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu  
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Asp Glu  
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Pro Phe Phe  
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg  
115 120 125

Ile Val Arg Phe Asp Val Ser Ala Met Glu Lys Asn Ala Ser Asn Leu  
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg  
145 150 155 160

Val Pro Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp  
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr  
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val His  
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu  
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro  
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr  
245 250 255

Ser Thr Tyr Thr Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys  
260 265 270

Lys Asn Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser  
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Thr Asn Arg Arg Lys Lys Arg Ala Leu  
290 295 300

Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg  
305 310 315 320

Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His  
325 330 335

Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr  
340 345 350

Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr Asn  
355 360 365

Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp  
370 375 380

Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro Lys Ile

385

390

395

400

Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser  
405 410

<210> 4  
<211> 412  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Lys Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn  
1 5 10 15

Phe Ala Thr Val Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe  
20 25 30

Gly His Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu  
35 40 45

Ser Lys Leu Arg Leu Thr Ser Pro Pro Glu Pro Thr Val Met Thr His  
50 55 60

Val Pro Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu  
65 70 75 80

Glu Glu Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Asn Thr  
85 90 95

Glu Ser Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln  
100 105 110

Gly Leu Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr  
115 120 125

Ser Lys Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Arg Thr  
130 135 140

Asn Leu Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser  
145 150 155 160

Ser Lys Arg Asn Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro  
165 170 175

Asp Glu His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro  
180 185 190

Thr Arg Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val  
195 200 205

Arg Glu Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser  
210 215 220

Ile His Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu  
225 230 235 240

Asn Ile His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu  
245 250 255

Asp Asp His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp  
260 265 270

His His Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu  
275 280 285

Asp Asn Pro Gly Gln Gly Gln Arg Lys Lys Arg Ala Leu Asp Thr  
290 295 300

Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu  
305 310 315 320

Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro  
325 330 335

Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg  
340 345 350

Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu  
355 360 365

Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu  
370 375 380

Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln  
385 390 395 400

Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser  
405 410

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<211> 18  
<212> PRT  
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<400> 5

Met Lys Trp Val Thr Phe Leu Leu Leu Phe Ile Ser Gly Ser Ala  
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Phe Ser

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<210> 7  
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<400> 7  
cgggtgttcg aatttagttt tgtattggaa ggg 33

<210> 8  
<211> 56  
<212> DNA  
<213> Homo sapiens

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<210> 9  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 9  
tagtctcgag ttatcagctg cacttgagg 30

<210> 10  
<211> 45

<212> DNA  
<213> Rattus rattus

<400> 10  
aaagggggat cgcaccat gaagtggta accttctcc tcctc 45

<210> 11  
<211> 45  
<212> DNA  
<213> Rattus rattus

<400> 11  
agaaaaaggca gaacccgaga tgaagaggag gaggagaaag gttac 45

<210> 12  
<211> 39  
<212> DNA  
<213> Sus scrofa scrofa

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cgccctcagtg cccactgttc ctgtgacagc aaagataac 39

<210> 13  
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<212> DNA  
<213> Sus scrofa scrofa

<400> 13  
gttatcttg ctgtcacagg aacagtgggc actgaggcg 39

<210> 14  
<211> 33  
<212> DNA  
<213> Sus scrofa scrofa

<400> 14  
ggatccctgt ccacctccaa gaccatcgac atg 33

<210> 15  
<211> 33  
<212> DNA  
<213> Sus scrofa scrofa

<400> 15  
catgtcgatg gtctggagg tggacagggta tcc 33

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<212> PRT  
<213> Artificial Sequence

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<223> Synthetic construct

<400> 16

His His His His His His Leu Ser Thr Ser Lys Thr Ile Asp  
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Met Glu Leu Val  
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<210> 17

<211> 20

<212> PRT

<213> Sus scrofa scrofa

<400> 17

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys  
1 5 10 15

Val Arg Gln Leu  
20